

RT-PCR Fold Change in Male HSD Rats

C12010-01 Drometrizole

Parameter ^a	Control	30 mg/kg	100 mg/kg	300 mg/kg	1000 mg/kg	Trend ^b
Kidney						
Havcr1	1.09 ± 0.24 (4)	0.97 ± 0.29 (5)	1.91 ± 0.47 (5)	2.53 ± 1.43 (4)	9.11 ± 4.38 (5)	0.016+
Liver						
Acot1	1.20 ± 0.27 (5)	1.07 ± 0.23 (4)	1.09 ± 0.20 (4)	1.22 ± 0.22 (4)	0.36 ± 0.15 (3)	0.134-
Acox1	1.01 ± 0.07 (5)	0.82 ± 0.16 (4)	0.70 ± 0.15 (5)	0.68 ± 0.03 (5) *	0.83 ± 0.03 (5)	0.243-
Ccng1	1.01 ± 0.08 (5)	1.30 ± 0.07 (4)	1.02 ± 0.08 (5)	0.93 ± 0.05 (5)	1.04 ± 0.05 (5)	0.509-
Cdkn1a	1.03 ± 0.13 (5)	1.01 ± 0.21 (4)	0.78 ± 0.13 (5)	1.00 ± 0.10 (5)	0.87 ± 0.07 (5)	0.509-
Cyp2b1	1.12 ± 0.25 (5)	1.93 ± 1.55 (4)	1.66 ± 0.54 (5)	0.69 ± 0.13 (5)	2.09 ± 0.77 (5)	0.839+
Cyp3a23/3a1	1.01 ± 0.09 (5)	0.96 ± 0.16 (4)	0.80 ± 0.15 (5)	0.78 ± 0.03 (5)	0.72 ± 0.07 (5)	0.037-
Cyp4a1	1.02 ± 0.11 (5)	0.81 ± 0.16 (4)	0.90 ± 0.20 (5)	0.67 ± 0.09 (5)	0.95 ± 0.37 (5)	0.075-
Gstm3	1.06 ± 0.18 (5)	1.11 ± 0.24 (4)	0.85 ± 0.20 (5)	0.85 ± 0.14 (5)	0.72 ± 0.16 (5)	0.104-
Nqo1	1.01 ± 0.06 (5)	0.93 ± 0.15 (4)	1.02 ± 0.12 (5)	1.17 ± 0.19 (5)	2.00 ± 0.57 (5)	0.017+

The RT-PCR fold change values were calculated from the base signal values using the $2^{-\Delta\Delta Ct}$ method.

Gapdh was used as the reference housekeeping gene.

a: Results shown as mean ± standard error (N)

b: Statistical analysis performed by Jonckheere (trend) and Shirley or Dunn (pairwise) tests.

* Statistically significant at $P \leq 0.05$

** Statistically significant at $P \leq 0.01$

Liver Cyp1b1 gene was excluded from the analysis.

Animal 200 Liver Acot1 gene was excluded from the analysis.

Animal 183 Liver genes were excluded from the analysis because of high Ct value for Gapdh.